

AMENDMENTS TO THE CLAIMS

1. (Currently amended) A transgenic expression ~~construct~~ construct for predominant expression of a nucleic acid sequence of interest in substantially all vegetative plant tissues comprising a promoter sequence selected from the group consisting of:

- a) the promoter of the *Pisum sativum* ptxA gene, functional equivalent fragments and functional equivalent homologs thereof, or their complements, having essentially the same promoter activity as the promoter of the *Pisum sativum* ptxA gene, and
- b) the promoter of the *Glycine max* extensin (SbHRGP3) gene, functional equivalent fragments and functional equivalent homologs thereof, or their complements, having essentially the same promoter activity as the promoter of the *Glycine max* extensin (SbHRGP3) gene,
wherein said promoter sequence is operably linked to a ~~the~~ nucleic acid sequence of interest to be transgenically expressed, and wherein said promoter sequence is heterologous with respect to said nucleic acid sequence of interest.

2. (Currently amended) The transgenic expression construct of Claim 1, wherein the promoter sequence is selected from the group of sequences consisting of:

- a) the promoter of the *Pisum sativum* ptxA gene as described by SEQ ID NO: 1, or its complement,
- b) a functional equivalent fragment of at least 50 consecutive base pairs of the promoter sequence described by SEQ ID NO: 1, or its complement, having essentially the same promoter activity as the promoter sequence described by SEQ ID NO: 1, and
- c) a functional equivalent homolog of the promoter sequence described by SEQ ID NO: 1 which has essentially the same promoter activity as the promoter sequence described by SEQ ID NO: 1, and ~~has~~
 - i) has a homology of at least 95% over a sequence of at least 100 consecutive base pairs to the sequence as described by SEQ ID NO: 1, and/or
 - ii) hybridizes under high stringency conditions with a fragment of at least 50 consecutive base pairs of the ~~nucleic acid molecule~~ sequence as described by SEQ ID NO: 1.

3. (Original) The transgenic expression construct of Claim 2, wherein the functional equivalent fragment comprises a sequence from about base pair 300 to about base pair 583 of the sequence described by SEQ ID NO: 1.
4. (Currently amended) The transgenic expression construct of Claim 1, wherein the promoter sequence is selected from the group of sequences consisting of:
 - a) the promoter of the *Glycine max* extensin (SbHRGP3) gene as described by SEQ ID NO: 2, or its complement,
 - b) a functional equivalent fragment of at least 50 consecutive base pairs of the promoter sequence described by SEQ ID NO: 2, or its complement, having essentially the same promoter activity as the promoter sequence described by SEQ ID NO: 2, and
 - c) a functional equivalent homolog of the promoter sequence described by SEQ ID NO: 2 which has essentially the same promoter activity as the promoter sequence described by SEQ ID NO: 2, and ~~has~~
 - i) has a homology of at least 60% over a sequence of at least 100 consecutive base pairs to the sequence as described by SEQ ID NO: 2, and/or
 - ii) hybridizes under high stringency conditions with a fragment of at least 50 consecutive base pairs of the ~~nucleic acid molecule~~ sequence as described by SEQ ID NO: 2.
5. (Original) The transgenic expression construct of Claim 4, wherein the functional equivalent fragment comprises a sequence from about base pair 800 to about base pair 1179 of the sequence described by SEQ ID NO: 2.
6. (Currently amended) The transgenic expression construct of Claim 4, wherein the functional equivalent homolog is described by a sequence selected from the group of sequences ~~described by~~ consisting of SEQ ID NO: 7, 8, and 9.
7. (Currently amended) The transgenic expression construct of ~~any of Claim 1 to 6~~ claim 1, wherein the expression rate realized by the transgenic expression construct and measured by an quantitative β -glucuronidase assay and normalized to units of β -glucuronidase per gram of

biomass in seed and flower tissue is less than 10% of the corresponding value in total vegetative plant tissue.

8. (Currently amended) The transgenic expression construct of ~~Claim 1 to 7~~ claim 1, wherein

- a) the nucleic acid sequence of interest to be expressed is linked operably to further genetic control sequences, or
- b) the expression construct comprises additional functional elements, or
- c) both a) and b) apply.

9. (Currently amended) The transgenic expression construct of ~~Claim 1 to 8~~ claim 1, wherein the nucleic acid sequence to be expressed transgenically results in,

- a) expression of a protein encoded by said nucleic acid sequence, and/or
- b) expression of sense, antisense, or double-stranded RNA encoded by said nucleic acid sequence.

10. (Currently amended) The transgenic expression construct of Claim 1 to 9, wherein expression occurs in leaves, stems and roots but is not detectable in seeds.

11. (Currently amended) A transgenic expression vector comprising ~~a~~ the transgenic expression construct of ~~any of~~ Claim 1 to 10 claim 1.

12. (Currently amended) A non-human transgenic organism transformed with ~~an~~ the expression construct as claimed in ~~any of claims 1 to 10 or a vector as claimed in~~ Claim 11 claim 1.

13. (Currently amended) The non-human transgenic organism of Claim 12, said organism is selected from the group consisting of bacteria, yeasts, fungi, animal and plant organisms.

14. (Currently amended) The non-human transgenic organism of Claim 13, wherein the organism is selected from the group consisting of sugarcane, maize, sorghum, pineapple, rice, barley, oat, wheat, rye, yam, onion, banana, coconut, date, hop, rapeseed, tobacco, tomato, tagetes (marigold), soybean, pea, common bean, and papaya.

15. (Currently amended) A cell culture, part or transgenic propagation material derived from a ~~the~~ transgenic organism of ~~Claim 12 to 14~~ claim 12.

16. (Currently amended) A method for producing transgenic predominant expression of a nucleic acid sequence of interest in substantially all vegetative plant tissues comprising:

i. ~~introduction of introducing~~ a transgenic expression construct into a plant cell or a plant, said transgenic expression construct ~~comprising~~ comprises a promoter sequence selected from the group consisting of:

a) the promoter of the *Pisum sativum* ptxA gene, functional equivalent fragments and functional equivalent homologs thereof, or their complements, having essentially the same promoter activity as the promoter of the *Pisum sativum* ptxA gene, and

b) the promoter of the *Glycine max* extensin (SbHRGP3) gene, functional equivalent fragments and functional equivalent homologs thereof, or their complements, having essentially the same promoter activity as the promoter of the *Glycine max* extensin (SbHRGP3) gene,

wherein said promoter sequence is operably linked to a ~~the~~ nucleic acid sequence of interest to be transgenically expressed, and wherein said promoter sequence is heterologous with respect to said nucleic acid sequence of interest,

under conditions such that said nucleic acid sequence of interest is expressed in said plant cell and/or predominantly expressed in the vegetative plant tissue and/or organs of said transgenic plant.

17. (Currently amended) The method of Claim 16, wherein the expression occurs in leafs, stems and roots but is not detectable in seeds.

18. (Currently amended) The method of Claim 16 or 17, said method further ~~comprising~~ comprises one or more of the following steps:

ii) identifying or selecting the transgenic plant cell comprising said transgenic expression construct,

iii) regenerating transgenic plant tissue from the transgenic plant cell, and

iv) regenerating a transgenic plant from the transgenic plant cell.

19. (Cancelled)

20. (Currently amended) ~~The use of a~~ A foodstuff, animal feeds, seeds, pharmaceuticals or fine chemicals produced from the transgenic organism as claimed in claim 12 to 14 or of cell cultures, parts of transgenic propagation material derived therefrom ~~as claimed in claim 15 for the production of foodstuffs, animal feeds, seeds, pharmaceuticals or fine chemicals.~~

21. (Currently amended) A method for production of a foodstuff, animal feed, seed, pharmaceutical or fine chemical, wherein the method comprises employing a the transgenic organism as claimed in claim 12 to 14 or of cell cultures, parts of transgenic propagation material derived therefrom ~~as claimed in claim 15.~~